FIG. 1A

			10						30	C						50			
TT	CGG	GCA(CGA	GGG	CAG		GGC	GCC	ACC	ACC	AGC'	rag.	AGT	ACA'	TCT	'AGG'	IGC	GTT	CCTG
						M_	<u>_A</u> _	<u> P</u>	_ <u>P</u>	P	<u>A</u>	R	V	<u>H</u>	L	<u>_G</u>	<u> A</u>	F	Ţ
		•	70						90	0						110			
GC	AGTY	GAC	ICC	GAA	TCC	CGG	GAG	CGC	AGC	GAG	TGG	GAC	AGA(GGC.	AGC	CGC	GGC(CAC	ACCC
A	V	ፗ	·P	N	P	G	S	_A	A	S	G	${f T}$	E	A	A	$_{i}\mathbf{A}$	A	${f T}$	P
		1:	30				_		150	n l						170			
AG	מבר	ΑĠͲϒ		GGG	СЩС	יאדיי	്ര	ഭവ		_	מבאדי	אררי	አ ርር:	مرحد		<i>-</i>	700	አርር	AGCG
	K	77	TAT	G	S	S	A	G	R	T	E	P	R			<i>l</i> _			
S	. 11.	7 1 6	90	G	.5	3	A	9	(21)	↑	Ŀ	P	ĸ	G	G	G	R	G	A
			7 U 7 W ~	~a m	~~~	3 (T 3)	~~~	~	17-	_		~~~	~~~	~~~	~_	230	~~~	~~~	~~~-
CI		TAC	JIC ~			_		_	11		TGC				GGC	AGG	3CG	CGC	CCCA
T	P	T	S	M	G	Q	H	G	P	\S	A	R	A	R	A	G	R	A	P
		2.	50						27	6/		•			/	290			
GG	ACC	CAG	GCC	GGC	GCG	GGA	AGC	CAG	CCC	ĭ Ç Ğ	GCT	CCG	GGT	CCX	CAA	GAC	CTT	CAA	GTTT
G	P	R	P	A	R	E	A	S	P	R	L.	R	V	H	K	${f T}$	F	K	F
		3:	10						330	0						350			
GT	CGT	CGTY	CGG	GGT	CCT	GCT	GCA	GGT	CGÀ	ACC	TAG	CTC	MGC'	TGC	AAC	САТ	CAA	АСТ	TCAT
V	V	V	G	V	L	T	0	V	V	/B	sl	S	A	A	ىل مەسى	Т	ĸ	Τ.	H
•	•	¸ ``\	70	•		_	×	•	39	1.15	I^{\sim}		11	11	*	410	10		11
CN	י אי־עד	ATC:	. •	ידעיר	ርአር	ACA	CCX	Nav.		- 1			/ ////// //	~~~	202	4T0	~~~	maa	3.003
D	\sim	aru	L COURT	100	CASC.	ACA		HAT G			TAG		T.T.T.	eren T	AGA	70.T.T.	2 <u>1</u> 6	TCC	ACCA
ע	Ž	<u>ې</u>		G	T	Q	Q 🕴	/ W	E	H	S	P	بل	G	E	با	C	P	P
			30					1 1	45	_						470			
GG.	ATC'	TCA'	rag	ATC	AGA	ACG	TCC	TGÇ	AÇC	CTĢ	TAA	CCG	GTG	CAC	AGA	YGGG.	IGT	GGG	TTAC
G	S	H	R	S	E	R	P	G`	AA A	_0″	N	R	C	${f T}$	E	G	V	G	Y
		4	90						51	Ō						530			
AC	CAA'	TGC'	TTC	CAA	CAA	TUL	GTT	ŦGC	TIG	CCT	CCC	ATG	TAC	AGC	TT	TAA	АТС	AGA	TGAA
\mathbf{T}	N	Α	S	N	N		F	A.	C	Τ.	P	~	T	A		K	S	ח	E
_	_,	<u>-</u> 5	50			~~~			57	^	-	•	-	**	_	590	٥		-
CΔ	אכם	GAG		ייתיים רי	تكست	CAC	CAC	CAC	_	_	C λ C	አራራ	א ווועריי	т стъ.	\sim m \sim		3 CC	3 CC	AACT
E	E	R	S	P	~	T	agr.	T.	1	. N			AIG		OIC A				
Ŀ	<u>r</u>			P	6	Τ.	T 4	A T	R		${f T}$	A	C	Q	Ç	K	P	G	${f T}$
	~~~		10	:	V			- 8	63			_				650			
.1.17		GAA'	TGA		TIG	ACC.	<b>TGA</b>	GAT	GIG	CCG	GAA	GTG	CAG	CAC	AGC	GTG	CCC	CAG	AGGG
F	R	N	Pį	N	S	Ą	E	W	~ C	R	K	C	S	${f T}$	G	C	P	R	G
		6	70						69	0						710			
AT	GGT	CAA	GG <b>¹</b> į́	CAA	.GGA	TTG	ŤĄC	GCC	CTG	GAG	TGA	CAT	<b>CGA</b>	GTG	TGI	CCA	CAA	AGA	ATCA
M	V	K	V	K	Þ	C	T	P	W	S	D	I	E	C	V	Н	K	E	S
		7.	30		- \			\	75	0			•	_		770	-		
GG	CAA	TGG	ACA	KAT	TA'	'ATG	GGT	ΥÄТ			<b>ጥርን</b> ሞ	GAC	TTT	വാവ	ጥረገጥ		ىلىك	COM	كليك
2	N	K	H.			\w	77	\/	Τ.	77	77	Tr.	T	77	77	D	T	T.	T.
					**	*/**	***	$k_{\star}^{\perp}$	* * *	* * *	***	* * *	***	<b>+</b> + +	* * *		* <b>+</b> *	***	****
		7		<b>∀</b> ,	4		,, -,	** ***	101	^		~ ~ ~	^ ^ ^	^ ^ ^	^ ^ ^				
۱	~~~	/ ~~~	90 			<u>.                                    </u>			81	_						830			
<b>\</b> GT	GGC	'IGI'	GC'I	GA'I	'IGT	CIG	A.Le	TIE	CAT	CGG	CTC	AGG	TTG	TGG	AGC	3GGA	CCC	CAA	GTGC
Y	A	V	L	I	V	C	É	C	I	G	S	G	C	G	G	D	P	K	C
*/*	* * *	* * *	* * *	* * *	* * *	***	* * *	***	***	***	***	* * *	**						
•		8	50				·	\	87	0						890			
AT	<b>G</b> GA	CAG	GGI	GTG	TTT	YTG	GCG	$C^{TT}$	<b>GGG</b>	тст	CCT	ACG	AGG	GCC	ጥርረ			GGA	CAAT
М		R	7.7		F	W	R	$I_{\rm L}$	G	Τ.	T.	R	G	P	G	A	E	D	N
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~~	<b>ДУ</b> ¬ Ъ				<b>Y</b> 70~10	<b>~~~</b>	'	~~~	$\frac{1}{2}$		·	∕~l~	·~ -		·~~	950		~~-	<i></i>
_			<b>L</b> GN	GAT	TAT				1_		.GCT	G.T.C	CAC	T.T.T.	CGT			.GCA	GCAA
A	H	N		I	L	S	N	A	D	S	L	S	${f T}$	F	V	S	E	Q	Q
			70	1					199							1010			
AT	GGA	AAG	CCA	<b>IGGA</b>	<b>ECC</b>	:GGC	AGA	TTT	<b>X</b> GAC	AGG	TGT	CAC	TGT	'ACA	GTC	CCC.	AGG	GGA	.GGCA
M	E	S	Q	E	P	A	D		m T	G	V	${f T}$	,V	0	S	Р	G	E	A

### FIG. 1B

		103	0						1050	)					10	70			
CA	GTGT	CTG	CTG	GGA:	CCG	GC2	AGAZ	\GC'	TGA	AGG(	STCI	CAC	GAGO	SAGO	AGC	CTC	CIX	GT.	rcca
Q	C	L :	L (	3	P	A	E	A	E	G	S	Q	R	R	R	L	L	V	P
		109	0						1110	)					11	L30			
GC	CAAA	CGGT	GCT	GAC	CCC	CAC	rga(	GAC	TCTY	YTAE	CTC	YPTE	CTT.	rgac	CAAC	HT.	rgcz	AAA(	CATC
A	N	G .	A I	0	P	$\mathbf{T}$	E	${f T}$	L	M	L	F	F	D	K	F	A	N	I
		115	0						1170	)					11	L90			
GT	GCC	TTT	GAC.	ICC	TGC	GA(	CCA	GCT	CATY	GAG(	<b>3CA</b> C	CIY	GGA(	CCIC	CACC	SAA	AAA	rga(	GATC
V	P	_	_	S	W	D	Q	$oldsymbol{L}$	M	R	Q	$oldsymbol{L}$	D	$oldsymbol{L}$	$T_{\perp}$	K	N	$\boldsymbol{E}$	I
,		121	_						1230							250			
GA'	TGT			_						_								-	AAA
D	V			A	G	T	A	G	P	Ğ	D	A	$oldsymbol{L}$	Y	$A_{\perp}$	M	L	M	K
	~~~	127	_						129	_		~~ ~.		~~~		310	~	~~~	~> ~~
	GGIY			ACT T												_			GAGG
W	V		K	T^{\cdot}	G	R	N	A	S		H	T	L	L_{\cdot}		A	L	\boldsymbol{E}	R
3 (7)	~~~	133	_	⇔	~~·		3 (13 A	~~~	135	_	~~~	7.CM	~~~			370	T	3	amma
AT M			_		A		AGAI E					CTV	L	V V	D D	S	G	AAA K	GTTC F
M	E	<i>E</i> 139		H	A	K	Ŀ	K	$rac{I}{141}$	Q ^	D	ш	ш	V	_	430	G	K	F
אתי	י מידיי		•	СЪТ	YZCZ	רארי	እርር	C		_	$\Box \Pi Y = 0$	الملتاب	CCA	CTYC	_		ተላ~ተቀ	Talala	TACC
T	V	T.	E 1	D Œ	.G	on G	roo F	S	A	77	S	T.	E	GIG	. 11 11 1	unc.	101		
		145		ט	3	_	-	٦	147	•	J				1.	490			
AG	AGG			מידים	\GG'	ጥርጥ	ጥልር፥	GAC		_	САТ	ידייים	AGG	ملململ			ململما	TTA.	ACAT
		151							153			_	_			550			
GT	ATA		_	raa	TC'	TTA	GCC	ACC		_	GGC'	TCC	TGC	CTG'	TAA'	TCC	CAT	CAC	TTTG
		157							159							610			
GG	AGG	CTGA	CGC	CGG	TG	GAT	CCA	CTI	GAG	GTC	CGA	AGT	TCC	AAG	ACC	AGC	CCT	GAA	CCAA
		163	0						165	0					1	670			
CA	.TCG	TGGA	TAA	GCC	CG	TCT	TTT	ACA	AAA	AAA	TAC	CAA	AAA	TTC	AAC	TGG	AAT	GTG	CATG
		169	0						171	0					1	730			
GT	GTG	TGCC	'ATC	ATI	TC	CTC	GGC	TAI	CTA	.CGG	GAG	GTC	TGA	.GGC	CAG	GAG	AAT	CCA	CTTG
		175	0						177	0				•	1	790			
AA	CCC			GAC	CAG	TGT	'AGA	CTC			GCA	CCA	.CTG	CAC				GGG	AACA
		181	_						183	_						850			
CA	GAG			CTC	FTC	TCA	AGA	TA.			ATA	AAC	TTG	AAA				CCC	GACT
		187	•						189	_						910			
GA	'GGC			iCC2	AA	.GÇA	AAA	TCI			CCC	CTG	AGC	'TGG		_		GTT	TCCT
		193				~~~			195	_		~~=				970			a conc
ΤA	ADTL			CAZ	7.T.L	GGA	GGT	GT.			AAT	GGA	ATTA	AGG				AAC	ACTG
~-		199	_	 -			~~~	-	201		.~~=	m~~	·	·~~		030		~ × ~	מאמרים
Ġ'I	:AAG			T.T.	J'I'G	رخن ه	CA'I	TA'.			iGCA	:1 G '1	C1'1	CGA.				UAU.	AGGG
<i>~</i>		205	· -	1 % cm2	7~~		107 P 0	1000 T	207		7 7 ~	3 ~~	1013 C	1/4/m		090		-	יכפאכ
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	יודעיי	211		יררי	~~~	יא ריר	17 7 C	י דרו אך א	213		. אאר	1 7 7 7 T	. T. T. T.	. א א א		150			
CGTCCGACAGACTGGGGAGCAAGATAGAAGAAAAAAAAAA																			

MEQRPRGCAAVAAALLULGARAQG - -MAPPPARVHLGAFLAVTPNPGSAASGTEAAAATPSKVWGS DR4 protein - L G D R E K R D S V C P Q G K Y I H P Q N N S I C T K C H K G T Y L Y N D C h TNFR I Protein -- GTRSPR-CDCA-GDF-HKKIGLFCCRGCPAGHYLKAPC DR3 protein SAGRIEPRGGGRGALPTSMGOHGPS----ARARAGRAPG DR4 protein PGPGQDTDCRECESGSFTASENHLR-HCLSCSKCRKEMGO h INFR I Protein
TEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASO DR3 protein PRPAREASPRLRVHKTFKFVVVGVLLQVVPSSAATIKLHD DR4 protein 55 DG----OFCHKP----CPPGERKARDCTVNGDEPDCVPCQ h Fas protein 112 VEISS ------CTVDRDTVCGC----PKNQYRHYW h TNFR I Protein
102 VALEN -----CSAVADTRCGC-----KPGWFVEC-DR3 protein
116 QSIGTQOWEHSPLGELCPPGSHRS-----ERPGACNRCT DR4 protein 87 EGKEYTDKAHFSSKCRRCRLCDEGHGLEVEINCTRTONTK h Fas protein 137 SENLFQC-----FNCSLCLN-GTVH----LSCQEKONTV h TNFR I Protein 126 -- QVSQCVSSSPEYCQPCLDCGALHR-HTRLLCSRRDTDC DR3 protein 150 EGVGYTNASNNLEACLPCTACKSDE--EERSPCTTTRNTA DR4 protein 127 CRCKPNFFCNSTVCEHCDPCTK-CEHGIIK--ECTLTSNT h Fas protein 166 CTCHAGFFLRE---NECVSCSN-CKKSLECTKLCLPQIEN h TNFR I Protein 163 GTCLPGFYEHG---DGCVSCPT-STLG-SCPERCAAVCGW DR3 protein
188 CQCKPGTFRNDNSAEMCRKCSTGCPRGMVKVKDCTPWSDI DR4 protein 164 KC-KEEGSRSNLGWLCL-----LLLPIPLIV----- h Fas protein 202 VKGTEDSGTTVLLPLVIFFGLCLLSLLFIGLM ----- h TNFR I Protein 198 RQ------ DR3 protein
228 ECVHKESGNGHNIWVILVVTLVVPLLLVAVLIVCCCIGSG DR4 protein ---- h Fas protein 234 -----YRYQR--WKSKLYSIVCGKSTPEKEGELEGTTTK h TNFR I Protein 222 -----YTYRHC-WPHKPL-VTADEAGMEALTPPPATHLS DR3 protein 268 CGGDPKCMDRVCFWRLGLLRGPGAEDNAHNEILSNADSLS DR4 protein 266 PLAPN PSFSPTPGFTPTLGFSPVPSSTFTSSSTYTPGD-C h TNFR I Protein 254 PLDSAHTLLAPPDSSEKICTVQLVGNSWTPGYPETQEALC DR3 protein 226 -----DVDLSKYITTIAGVMTLSQVKGFVRKNGVNEA h Fas protein 345 AHKPQSLDTDDPATLYAVVENVPPL-RWKEFVRRLGLSDH h TNFR I Protein 322 AGSPAMMLQPGPQ-LYDVMDAVPAR-RWKEFVRTLGLREA DR3 protein 363 -----TLML--FFDKFANIVPFDSWDQLMRQLDLTKN DR4 protein 258 KIDEIKNDNVQDTAEQKVQLLRNWHOLHGKKEA-YDTLIK h Fas protein 384 EIDRLELQNGRCLREAQYSMLATWRRRTPRREATLELLGR h TNFR I Protein 360 EIEAVEVEIGR-FRDQOYEMLKRWROQOP---AGLGAVYA DR3 protein 393 ETD VVRAGTA-GPGDALYAMLMKWVNKTGRNAS-IHTLLD DR4 protein 297 DIKKANICTLAEKIOTIILKDITSDSENSNFRNEIQSLV h Fas protein 424 VLRDMDLLGCLEDIE EAL -----CGPAALPPAPSLLR h TNFR I Protein 396 ALERMGLDGCVEDL------RSRLQRGP 431 ALERMEERHAKEKIODLLVDSGKFIYLEDGTGSAVSLE DR3 protein DR4 protein

FIG. 2B

1 1 1		LELLVGIYPSGVIGLVPH	
7 34 27 41	- L G D R II II R D S V C P Q C - G T P II I R - C D C A - C S A G R I II I R G G G R G A I	PLVLTSVARL-SSKSVNSKYIHPONNSICCTKCHKGTYLYNDC BDF-HKKIGLFCCRGCPAGHYLKAPC PTSMGOHGPSARARAGRAPG	h Fas protein h TNFR I Protein DR3 protein DR4 protein
25 73 62 76	AQVTDINRKGLELRI PGPGQIITDCRECESO TEPCGIITCLVCPQI PRPARMASPRLRVHI	TVTTVETONLEG	h Fas protein h TNFR I Protein DR3 protein DR4 protein
112 · 102 116	VEISS VALEN QSIGTUNWEHSPLGI	- C P P G E R K A R D C T V N G D E P D C V P C Q - C T V D R D T V C G C R K N Q Y R H Y W - C S A V A D T R C G C K P G W F V E C - E L C P P G S H R S E R P G A C N R C T	h TNFR I Protein DR3 protein DR4 protein
		CRRCRLCDEGHGLEVEINCTRTQNTKCSLCLN-GTVHLSCQEKONTVCQPCLDCGALHR-HTRLLCSRRDTDCLPCTACKSDEEERSPCTTRNTA	
166 163 188	CTCHAIIPPLRE I GTCLPIIPPRNDNSA CQCKPIIPRNDNSA	EHCDPCTK-CEHGIIKECTLTSNT NECVSCSN-CKKSLECTKLCLPQIEN DGCVSCPT-STLG-SCPERCAAVCGW EMCRKCSTGCPRGMVKVKDCTPWSDI	h TNFR I Protein DR3 protein DR4 protein
198 228	ECVHK R R G N G H N I W	LCL	DR3 protein DR4 protein
189 234 222 268		K S K L Y S I V C G K S T P E K E G E L E G T T T K P H K P L - V T A D E A G M E A L T P P P A T H L S R L G L L R G P G A E D N A H N E I L S N A D S L S	h Fas protein h TNFR I Protein DR3 protein DR4 protein
		T PT LGFSP V P S S T F T S S S T Y T P G D - C S E K I C T V Q L V G N S W T P G Y P E T Q E A L C D L T G V T V O S P G E A Q C	
200 305 294 337	RKHRK PNFAAI'RREVAPPY PQVTWINDQLPS ILGPA	ENQGSHESPTLNPETVAINLS QGADP.ILATALASDPIPNPLQKWEDS RALGPAAAPTLSPESP EAEGSQRRRLLVPANGADPTE	h Fas protein h TNFR I Protein DR3 protein DR4 protein
345 322 363	AHKPQ 11.1 DTDDPAT AGSPANNLQPGPQ - - TLML	Y I T T I A G V M T L S Q V K G F V R K N G V N E A L Y A V V E N V P P L - R W K E F V R R L G L S D H L Y D V M D A V P A R - R W K E F V R T L G L R E A F F D K F A N I V P F D S W D Q L M R Q L D L T K N	h TNFR I Protein DR3 protein DR4 protein
258 384 360 393	KIDEIKNDNVQDTA EIDRLELQNGRCLR EIEAVEVEIGR-FR EIDVVIIAGTA-GPG	E Q K V Q L L R N W H Q L H G K K E A - Y D T L I K E A Q Y S M L A T W R R R T P R R E A T L E L L G R D Q O Y E M L K R W R O Q Q P A G L G A V Y A D A L Y A M L M K W V N K T G P N A S - I H T L L D	h Fas protein h TNFR I Protein DR3 protein ER4 protein
297 424 396 431	DLKKANICTLAEKI VLRDMIIILGCLEDI ALERMIIDGCVEDL ALERMEERHAKEKI	OTIILKDITS DS ENSN FRNE I QS LV E E A L C G P A A L P P A P S L L R R S R L Q R G P O D L L V D S G K F I Y L E D G T G S A V S L E	h Fas protein h TNFR I Protein DR3 protein DR4 protein

Figure 3

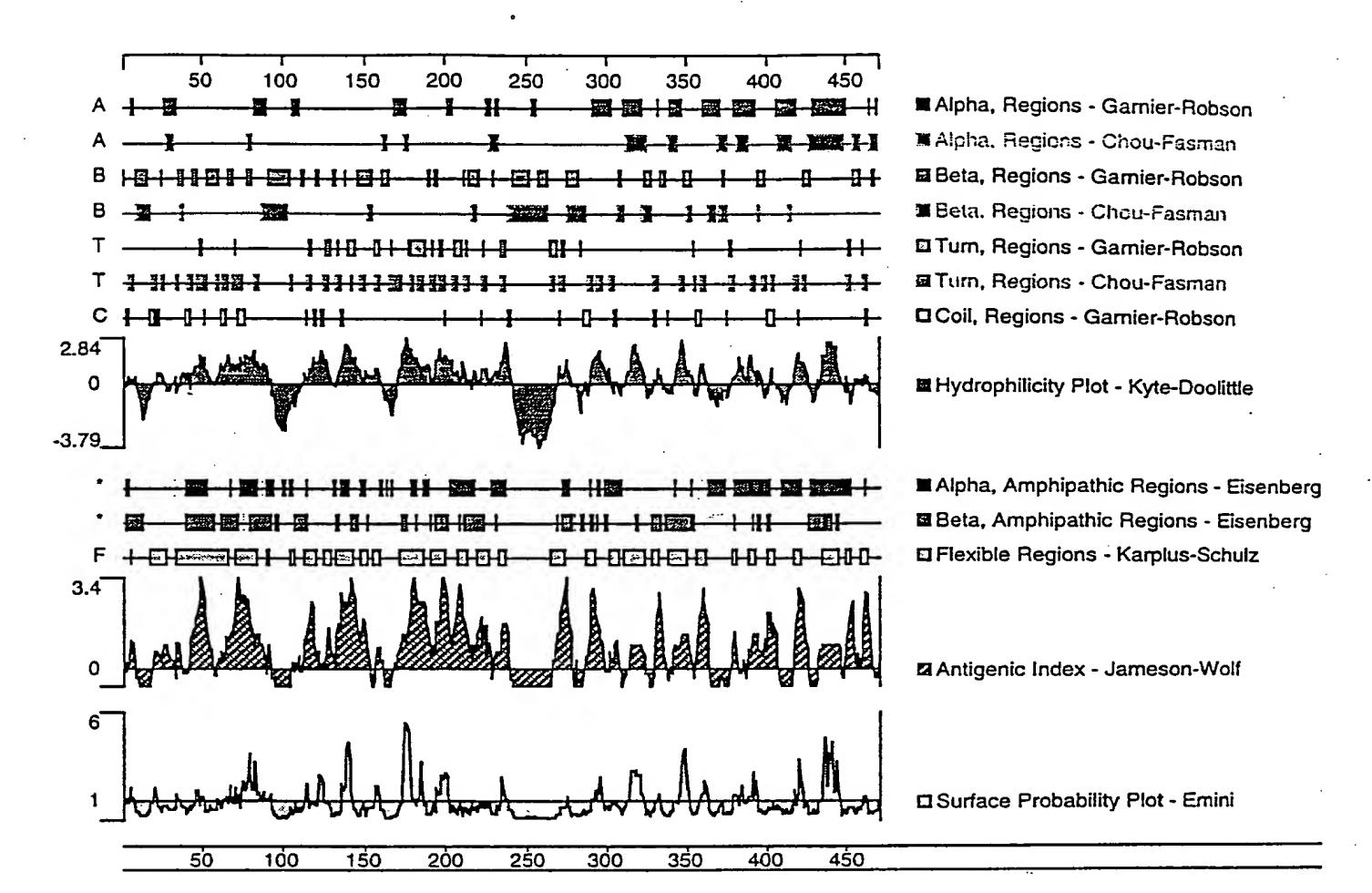


FIG. 4A

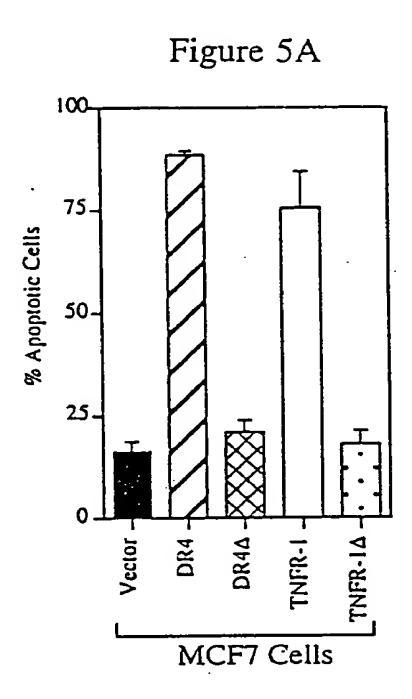
HTOIY07R

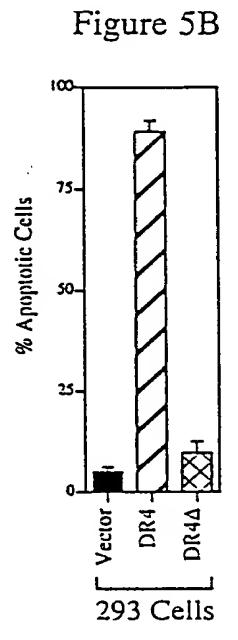
1	GGCANAGGTN	CGTACCTAGC	TCACCTGCAA	CCATCAAACT	TNATGATCAA
51	TCAATTGGCA	CACAGCAATG	GGAAACATAG	CCCTTTGGAA	GANTTGTNTC
101	CACCAGGATC	TCATAGATCA	AAACATCCTG	GGAGCCTGTT	AACCGGTGCC
151	CCAAAGGNTG	GTCAAGGTCA	AGGAATTGTT	NCGCCCTGGA	AGTGAACATC
201	GAGTGTNTCC	ACAAAGGATT	CAGGCAATGG	GACATAAATA	TATGGGTGAA
251	TTTTGGTTGT	GAACTTTGGT	TGNTCCCGTT	GNTGTTGNTG	GCTGTGCTGA
301	TTGTTTGTTG	TTGCATCGGC	TTCAGGTTNT	GGAGGGGGAC	CCAAGTGCAT
351	GGACAGGGTG	TGTTTCTGGG	GTTTGGGTCT	CTTAGAGGGC	NTGGGTTANG
401	CCANCTTCAC	ል ል ርርርርጥጥጥጥል	CCAANC	•	

FIG. 4B

HTXEY80R

1	TGGGGCTGAG	GACAATGCTG	ACNACGAGAT	TCTGAGCAAC	GCAGNACTNG
51	CTGTCCACTT	TCGTCTNTGN	GCAGCAAATG	GAAAGCCAGG	AGCCGGCAGA
101	TTTGACAGGT	GTCACTGTAC	AGTCCCCAGG	GGAGGCACAG	TGTCTGCTGG
151	TGAGTTGGGG	ACAGGCCCTT	GCAAGACCTT	GTGAGGCAGG	GGGTGAAGGC
201	CATGNCTCGG	CTTCNNNTGG	TCAAAGGGGA	AGTGGAGCCT	GAGGGAGATG
251	GGACTTNAGG	GGGACGGNGC	TGCGTGGGGA	AAAAGCAGCC	ACCNTTTGAC
301	AAGGGGGACA	GGCATTTTTN	CAAATGTGTG	CTTNTTGGT	





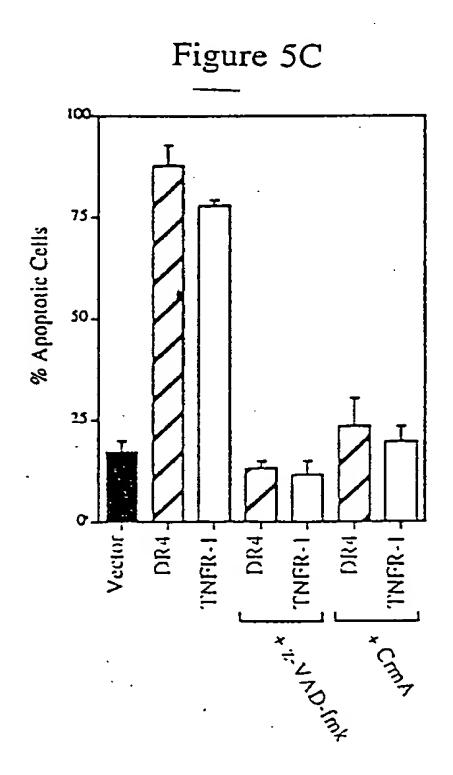


Figure 6A

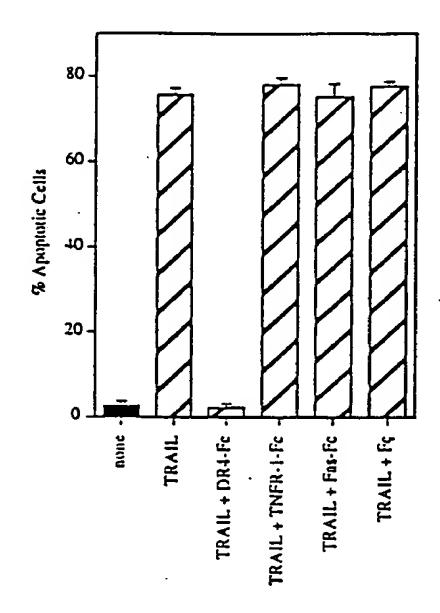


Figure 6B

